Classical segmentation methods on novel MR imaging: a study of brain tissue segmentation of MP2RAGE vs MPRAGE

Meritxell Bach Cuadra[1,2], Sebastien Gelin[2,3], Alexis Roche[1,4], Oscar Esteban[2,5], Tobias Kober[4], Jose Marques[6], Cristina Granziera[7], and Gunnar Krüger[4,8]

[1]Radiology Department, University Hospital Center (CHUV) and University of Lausanne (UNIL), Lausanne, Vaud, Switzerland, [2]Signal Processing Laboratory (LTS5), Ecole Polytechnique Fédérale de Lausanne (EPFL), Lausanne, Vaud, Switzerland, [3]Bern University, Bern, Bern, Switzerland, [4]Advanced Clinical Imaging Technology, Siemens Healthcare Sector IM&WS S, Lausanne, Vaud, Switzerland, [5]Biomedical Image Technologies (BIT), Universidad Politécnica de Madrid, Madrid, Madrid, Spain, [6]CIBM-Animal Imaging and Technology core, University of Lausanne, Lausanne, Vaud, Switzerland, [7]Department of Clinical Neurosciences, University Hospital Center (CHUV) and University of Lausanne (UNIL), Lausanne, Vaud, Switzerland, [8]CIBM-AIT, Ecole Polytechnique Fédérale de Lausanne (EPFL), Lausanne, Vaud, Switzerland

INTRODUCTION – Computer-based quantitative analysis of magnetic resonance (MR) imaging is increasingly used in clinical practice for providing diagnostic and prognostic biomarkers of brain diseases. To this end, significant effort has been made in the medical image processing community to develop robust and accurate brain tissue segmentation methods. While existing segmentation methods are mainly geared towards conventional T1-weighted images (e.g. MPRAGE), recent clinical research has highlighted the benefits of other image acquisition techniques (e.g. MP2RAGE[1]) to study the human brain anatomy. However, the applicability of existing tissue segmentation methods on novel MR sequences remains unknown.

PURPOSE – MP2RAGE has proven to be a bias-free MR acquisition with excellent contrast between grey and white matter. We investigated the ability of three state-of-the-art algorithms to automatically extract white matter (WM), grey matter (GM) and cerebrospinal fluid (CSF) from MPRAGE and MP2RAGE images: unified Segmentation (S) in SPM8[2], its extension New Segment (NS), and an in-house Expectation-Maximization Markov Random Field tissue classification[3] (EM-MRF) with Graph Cut (GC) optimization[4]. Our goal is to quantify the differences between MPRAGE and MP2RAGE-based brain tissue probability maps.

METHODS – For a detailed description of each tissue classification algorithm we refer the reader to[2,3,4]. In summary, the three main methodological differences are: 1) a 3-class model (CSF, GM and WM) within the brain (each class modelled by a mixture of two Gaussian distributions) is used in SPM8 (both S and NS) while a 5-class model (3 pure tissues plus CSF-GM and GM-WM partial volume, with one Gaussian distribution each) is implemented in EM-MRF; 2) SPM8 methods make use of brain tissue a priori probability maps registered from an atlas, while EM-MRF uses an atlas-free smoothness enforcing prior; 3) New Segment includes an improved registration model and different use of mixing proportions of the atlas priors as compared to Segment. **Data**: Imaging was performed on 19 healthy subjects (25 to 60 yo) at 3T (MAGNETOM Trio a Tim System, Siemens Healthcare, Germany) with a 32-channel head array. MPRAGE parameters were 1x1x1.2*mm* voxel size, TI/TR=900/2300*ms,* flip angle=9° (iPAT=2, 5:12 *min*)[5]; MP2RAGE parameters were 1x1x1.2*mm* voxel size, TI1/TI2/TR=700/2500/5000*ms*, flip angles=4°/5°(iPAT=3, 8:42 *min*). **Processing**: default parameters and SPM8 built-in probabilistic atlases were used for S and NS, no bias correction was applied to MP2RAGE. The EM-MRF algorithm used the brain masks created using New Segment on the MPRAGE images. The same masks were used to remove the background in the MP2RAGE images.

RESULTS – Voxel-wise statistical analyses were performed using SPM8: Fig.1 shows the paired t-test (with age as covariate) on tissue probability maps with 6mm spatial smoothing. Corrections for multiple comparisons were performed by controlling the family-wise error rate at 5%. Clusters smaller than 25 voxels are not reported. For SPM-based methods, the GM probability is significantly higher for MP2RAGE in the putamen (S and NS) and the cerebellum (NS). EM-MRF shows higher GM probability for MP2RAGE in the putamen, the cerebellum and some cortical areas. The differences between SPM8 and EM-MRF likely arise from the different segmentation priors (atlas-based versus local spatial priors). On the other hand, the three methods found $WM_{MPRAGE} > WM_{MP2RAGE}$ in the cerebellum area only. No significant areas were detected when testing $GM_{MPRAGE} > GM_{MP2RAGE}$ or $WM_{MPRAGE} < WM_{MP2RAGE}$.

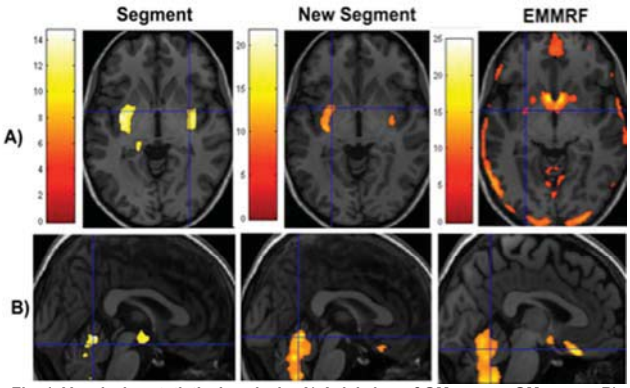

Fig. 1. Voxel-wise statistical analysis: A) Axial view of $GM_{MPRAGE} < GM_{MP2RAGE}$, B) Sagittal view of $WM_{MPRAGE} > WM_{MP2RAGE}$.

DISCUSSION – Existing brain tissue segmentation methods can successfully be applied to MP2RAGE data. Visual inspection of the EMMRF results (Fig.2) shows a better GM segmentation in the putamen, some cortical areas and cerebellum with the MP2RAGE sequence. Overall, segmentation results tend to be better using MP2RAGE despite segmentation algorithms are optimized for MPRAGE. This may be explained by better GM-WM contrast provided by MP2RAGE. As it is unlikely that SNR limits bias the results, the same findings are expected with a MPRAGE acquired without iPAT, i.e. with approx. the same acquisition time as the MP2RAGE protocol. Finally, we have observed that MP2RAGE intensity distribution of deep GM has less overlap with cortical GM than in the classical ADNI MPRAGE protocol. Existing segmentation models could therefore be modified to better account for this.

CONCLUSION – Our study suggests that MP2RAGE contrast may support a more accurate determination of structural changes arising from neurological diseases and thus it deserves to be further investigated in the context of brain morphometry.

REFERENCES – [1] Marques et al., Neuroimage 49(2):1271-1281 (2010); [2] Ashburner et al., NeuroImage 26(3):839-851 (2005); [3] Bach et al., IEEE TMI 25(2):241(2006); [4] Boykov et al., IEEE PAMI 26(9):1124-1137(2004); [5] Jack et al., Alzheimers Dement. 6(3):212-20 (2010).

This work was supported by CIBM of the UNIL, UNIGE, HUG, CHUV, EPFL and the Leenaards and Jeantet Foundations.

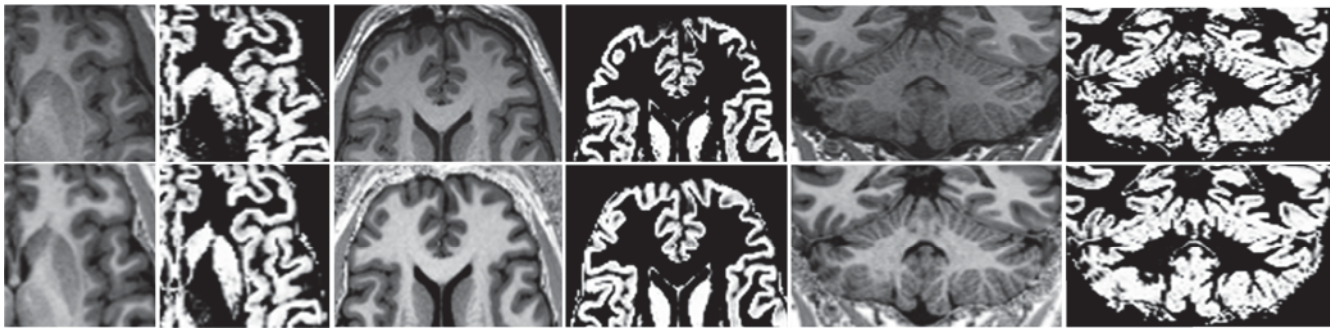

Fig. 2. Top row: MPRAGE, bottom row: MP2RAGE. GM segmentation with EM-MRF approach. Two first columns: putamen area; two middle columns: cortical GM in the frontal lobe; two right columns: cerebellum.